

## SEQUENCE LISTING

<110> Sundaresan, Venkatesan  
Tantikanjana, Titima

<120> Gene Controlling Shoot Branching in Plants

<130> 2577-135

<140> Not Yet Assigned

<141> 2000-05-01

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1614

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1611)

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ttt atc ctc tcc atg gca tca atc act cta ctg ggt cga ata ctc tca 96  
Phe Ile Leu Ser Met Ala Ser Ile Thr Leu Leu Gly Arg Ile Leu Ser  
20 25 30

agg ccc acc aaa acc aaa gac cga tct tgc cag ctt cct cct ggc cca 144  
Arg Pro Thr Lys Thr Lys Asp Arg Ser Cys Gln Leu Pro Pro Gly Pro  
35 40 45

cca gga tgg ccc atc ctc ggc aat cta ccc gaa cta ttc atg act cgt 192  
Pro Gly Trp Pro Ile Leu Gly Asn Leu Pro Glu Leu Phe Met Thr Arg  
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cct agg tcc aaa tat ttc cgc ctt gcc atg aaa gag cta aaa aca gat 240  
Pro Arg Ser Lys Tyr Phe Arg Leu Ala Met Lys Glu Leu Lys Thr Asp  
65 70 75 80

ata gca tgt ttc aac ttt gcc ggc atc cgt gcc atc acc ata aac tcc 288  
 Ile Ala Cys Phe Asn Phe Ala Gly Ile Arg Ala Ile Thr Ile Asn Ser  
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gac gag agc gct aga gaa gcg ttt aga gag cga gac gca gat ttg gca 336  
 Asp Glu Ser Ala Arg Glu Ala Phe Arg Glu Arg Asp Ala Asp Leu Ala  
           100                  105                  110

gac cgg cct caa ctt ttc atc atg gag aca atc gga gac aat tac aaa 384  
 Asp Arg Pro Gln Leu Phe Ile Met Glu Thr Ile Gly Asp Asn Tyr Lys  
           115                  120                  125

tca atg gga att tca ccg tac ggt gaa caa ttc atg aag atg aaa aga 432  
 Ser Met Gly Ile Ser Pro Tyr Gly Glu Gln Phe Met Lys Met Lys Arg  
           130                  135                  140

gtg atc aca acg gaa att atg tcc gtt aag acg ttg aaa atg ttg gag 480  
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           145                  150                  155                  160

gct gca aga acc atc gaa gcg gat aat ctc ata gct tac gtt cac tcc 528  
 Ala Ala Arg Thr Ile Glu Ala Asp Asn Leu Ile Ala Tyr Val His Ser  
           165                  170                  175

atg tat caa cgg tcc gag acg gtc gat gtt aga gag ctc tcg agg gtt 576  
 Met Tyr Gln Arg Ser Glu Thr Val Asp Val Arg Glu Leu Ser Arg Val  
           180                  185                  190

tat ggt tac gca gtg acc atg cga atg ttg ttt gga agg aga cat gtt 624  
 Tyr Gly Tyr Ala Val Thr Met Arg Met Leu Phe Gly Arg Arg His Val  
           195                  200                  205

acg aaa gaa aac gtg ttt tct gat gat gga aga cta gga aac gcc gaa 672  
 Thr Lys Glu Asn Val Phe Ser Asp Gly Arg Leu Gly Asn Ala Glu  
           210                  215                  220

aaa cat cat ctt gag gtg att ttc aac act ctt aac tgt tta ccg agt 720  
 Lys His His Leu Glu Val Ile Phe Asn Thr Leu Asn Cys Leu Pro Ser  
           225                  230                  235                  240

ttt agt cca gcg gat tac gtg gaa cga tgg ttg aga ggt tgg aat gtt 768  
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gat ggt caa gag aag agg gtg aca gag aac tgt aac att gtt cgt agt 816

Asp Gly Gln Glu Lys Arg Val Thr Glu Asn Cys Asn Ile Val Arg Ser  
 260 265 270

tac aac aat ccc ata atc gac gag agg gtc cag ttg tgg agg gaa gaa 864  
 Tyr Asn Asn Pro Ile Ile Asp Glu Arg Val Gln Leu Trp Arg Glu Glu  
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ggc ggt aag gct gct gtt gaa gat tgg ctt gat acg ttc att acc cta 912  
 Gly Gly Lys Ala Ala Val Glu Asp Trp Leu Asp Thr Phe Ile Thr Leu  
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aaa gat caa aac gga aag tac ttg gtc aca cca gac gaa atc aaa gct 960  
 Lys Asp Gln Asn Gly Lys Tyr Leu Val Thr Pro Asp Glu Ile Lys Ala  
 305 310 315 320

caa tgc gta gaa ttt tgt ata gca gcg att gat aat ccg gca aat aac 1008  
 Gln Cys Val Glu Phe Cys Ile Ala Ala Ile Asp Asn Pro Ala Asn Asn  
 325 330 335

atg gag tgg aca ctt ggg gaa atg tta aag aac ccg gag att ctt aga 1056  
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aaa gct ctg aag gag ttg gat gaa gta gtt gga aga gac agg ctt gtg 1104  
 Lys Ala Leu Lys Glu Leu Asp Glu Val Val Gly Arg Asp Arg Leu Val  
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gaa aca ttc aga att cac cca agt gct cat tat gtc cct tcc cat ctt 1200  
 Glu Thr Phe Arg Ile His Pro Ser Ala His Tyr Val Pro Ser His Leu  
 385 390 395 400

gcg cgt caa gat acc acc ctt ggg ggt tat ttc att ccc aaa ggt agc 1248  
 Ala Arg Gln Asp Thr Thr Leu Gly Gly Tyr Phe Ile Pro Lys Gly Ser  
 405 410 415

cac att cat gta tgc cgc cct gga cta ggt cgt aac cct aaa ata tgg 1296  
 His Ile His Val Cys Arg Pro Gly Leu Gly Arg Asn Pro Lys Ile Trp  
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 Lys Asp Pro Leu Val Tyr Lys Pro Glu Arg His Leu Gln Gly Asp Gly

435                      440                      445

atc aca aaa gag gtt act ctg gtg gaa aca gag atg cgt ttt gtc tcg 1392  
Ile Thr Lys Glu Val Thr Leu Val Glu Thr Glu Met Arg Phe Val Ser  
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ttt agc acc ggt cga cgt ggc tgc atc ggt gtt aaa gtc ggg acg atc 1440  
Phe Ser Thr Gly Arg Arg Gly Cys Ile Gly Val Lys Val Gly Thr Ile  
465                      470                      475                      480

atg atg gtt atg ttg ttg gct agg ttt ctt caa ggg ttt aac tgg aaa 1488  
Met Met Val Met Leu Leu Ala Arg Phe Leu Gln Gly Phe Asn Trp Lys  
485                      490                      495

ctc cat caa gat ttt gga ccg tta agc ctc gag gaa gat gat gca tca 1536  
Leu His Gln Asp Phe Gly Pro Leu Ser Leu Glu Glu Asp Asp Ala Ser  
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ttg ctt atg gct aaa cct ctt cac ttg tcc gtt gag cca cgc ttg gca 1584  
Leu Leu Met Ala Lys Pro Leu His Leu Ser Val Glu Pro Arg Leu Ala  
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Arg Pro Thr Lys Thr Lys Asp Arg Ser Cys Gln Leu Pro Pro Gly Pro  
35                      40                      45

Pro Gly Trp Pro Ile Leu Gly Asn Leu Pro Glu Leu Phe Met Thr Arg  
50                      55                      60

Pro Arg Ser Lys Tyr Phe Arg Leu Ala Met Lys Glu Leu Lys Thr Asp  
65                70                75                80

Ile Ala Cys Phe Asn Phe Ala Gly Ile Arg Ala Ile Thr Ile Asn Ser  
                  85                90                95

Asp Glu Ser Ala Arg Glu Ala Phe Arg Glu Arg Asp Ala Asp Leu Ala  
                  100                105                110

Asp Arg Pro Gln Leu Phe Ile Met Glu Thr Ile Gly Asp Asn Tyr Lys  
                  115                120                125

Ser Met Gly Ile Ser Pro Tyr Gly Glu Gln Phe Met Lys Met Lys Arg  
                  130                135                140

Val Ile Thr Thr Glu Ile Met Ser Val Lys Thr Leu Lys Met Leu Glu  
145                150                155                160

Ala Ala Arg Thr Ile Glu Ala Asp Asn Leu Ile Ala Tyr Val His Ser  
                  165                170                175

Met Tyr Gln Arg Ser Glu Thr Val Asp Val Arg Glu Leu Ser Arg Val  
                  180                185                190

Tyr Gly Tyr Ala Val Thr Met Arg Met Leu Phe Gly Arg Arg His Val  
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Thr Lys Glu Asn Val Phe Ser Asp Asp Gly Arg Leu Gly Asn Ala Glu  
                  210                215                220

Lys His His Leu Glu Val Ile Phe Asn Thr Leu Asn Cys Leu Pro Ser  
225                230                235                240

Phe Ser Pro Ala Asp Tyr Val Glu Arg Trp Leu Arg Gly Trp Asn Val  
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Asp Gly Gln Glu Lys Arg Val Thr Glu Asn Cys Asn Ile Val Arg Ser  
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Tyr Asn Asn Pro Ile Ile Asp Glu Arg Val Gln Leu Trp Arg Glu Glu  
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Gly Gly Lys Ala Ala Val Glu Asp Trp Leu Asp Thr Phe Ile Thr Leu  
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Lys Asp Gln Asn Gly Lys Tyr Leu Val Thr Pro Asp Glu Ile Lys Ala  
305 310 315 320

Gln Cys Val Glu Phe Cys Ile Ala Ala Ile Asp Asn Pro Ala Asn Asn  
325 330 335

Met Glu Trp Thr Leu Gly Glu Met Leu Lys Asn Pro Glu Ile Leu Arg  
340 345 350

Lys Ala Leu Lys Glu Leu Asp Glu Val Val Gly Arg Asp Arg Leu Val  
355 360 365

Gln Glu Ser Asp Ile Pro Asn Leu Asn Tyr Leu Lys Ala Cys Cys Arg  
370 375 380

Glu Thr Phe Arg Ile His Pro Ser Ala His Tyr Val Pro Ser His Leu  
385 390 395 400

Ala Arg Gln Asp Thr Thr Leu Gly Gly Tyr Phe Ile Pro Lys Gly Ser  
405 410 415

His Ile His Val Cys Arg Pro Gly Leu Gly Arg Asn Pro Lys Ile Trp  
420 425 430

Lys Asp Pro Leu Val Tyr Lys Pro Glu Arg His Leu Gln Gly Asp Gly  
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Ile Thr Lys Glu Val Thr Leu Val Glu Thr Glu Met Arg Phe Val Ser  
450 455 460

Phe Ser Thr Gly Arg Arg Gly Cys Ile Gly Val Lys Val Gly Thr Ile  
465 470 475 480

Met Met Val Met Leu Leu Ala Arg Phe Leu Gln Gly Phe Asn Trp Lys  
485 490 495

Leu His Gln Asp Phe Gly Pro Leu Ser Leu Glu Glu Asp Asp Ala Ser  
500 505 510

Leu Leu Met Ala Lys Pro Leu His Leu Ser Val Glu Pro Arg Leu Ala  
515 520 525

Pro Asn Leu Tyr Pro Lys Phe Arg Pro  
530 535